

WEST Search History

 09/SSS,529

DATE: Monday, October 29, 2007

Hide?	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L10	L8 not L9	21
<input type="checkbox"/>	L9	L7 and L8	2
<input type="checkbox"/>	L8	(kin17 or hskin17 or "kin 17")	23
<input type="checkbox"/>	L7	(kannouche-p\$.in. or mauffrey-p\$.in. or pinon-lataillade-g\$.in. or biard-d\$.in. or angulo-mora-j\$.in.)	21
<input type="checkbox"/>	L6	"COMMISSARIAT L-ENERGIE ATOMIQUE"!	1
<input type="checkbox"/>	L5	"COMMISSARIAT A. L-ENERGIE ATOMIQUE"!	0
<input type="checkbox"/>	L4	"COMMISSARIAT A L-ENERGIE ATOMIQUE"!	0
<input type="checkbox"/>	L3	"COMMISSARIAT A L-ENERGIE ATOMIQUED"!	0
<input type="checkbox"/>	L2	"COMMISSARIAT A L-ENERGIE ATOMIQUE"!	0
<input type="checkbox"/>	L1	"COMMISSARIAT A L-ENERGE ATOMIQUE"!	0

END OF SEARCH HISTORY

Alignment of SEQ ID NO: 2S
w/ Angulo et al

RESULT 1

S18666

KIN17 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S18666; A43753; SI4622

R;Angulo, J.F.; Rouer, E.; Mazin, A.; Mattei, M.G.; Tissier, A.; Horellou, P.; Benarous, R.; Devoret, R.

Nucleic Acids Res. 19, 5117-5123, 1991

A;Title: Identification and expression of the cDNA of KIN17, a zinc-finger gene located on mouse chromosome 2, encoding a new DNA-binding protein.

A;Reference number: S18666; MUID:92020193; PMID:1923796

A;Accession: S18666

A;Molecule type: mRNA

A;Residues: 1-391 <ANG>

A;Cross-references: UNIPROT:Q8K339; UNIPARC:UPI000017993F; EMBL:X58472

R;Angulo, J.; Rouer, E.; Benarous, R.; Devoret, R.

Biochimie 73, 251-256, 1991

A;Title: Identification of a mouse cDNA fragment whose expressed polypeptide reacts with anti-reCA antibodies.

A;Reference number: A43753; MUID:91355299; PMID:1715759

A;Accession: A43753

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 74-273 <ANW>

A;Cross-references: UNIPARC:UPI0000179940

C;Superfamily: KIN17 protein

Query Match 99.6%; Score 2020; DB 2; Length 391;
Best Local Similarity 99.5%; Pred. No. 3.7e-115;
Matches 389; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGKSDFLSPKAIANRIKSKGLQKLRWYCQMCQKQCRDENGFKCHCMSESHQRQLLASEN 60

Db 1 MGKSDFLSPKAIANRIKSKGLQNRWYCQMCQKQCRDENGFKCHCMSESHQRQLLASEN 60

Qy 61 PQQFMDYFSEEFRNDFLELLRRRFGTKRVHNNIVYNEYISHREHIHMNATQWETLTDFTK 120

Db 61 PQQFMDYFSEEFRNDFLELLRRRFGTKRVHNNIVYNEYISHREHIHMNATQWETLTDFTK 120

Qy 121 WLGREGLCKVDETPKGWYIIQYIDRDPETIRRQLELEKKKKQDLDDEEKTAKFIEEQVRRG 180

Db 121 WLGREGLCKVDETPKGWYIIQYIDRDPETIRRQLELEKKKKQDLDDEEKTAKFIEEQVRRG 180

Qy 181 LEGKEQETPVFTELSRENEEEKVTFNLNKGAGGSAGATTSKSSLGPSALKLLGSAASGK 240

Db 181 LEGKEQETPVFTELSRENEEEKVTFNLNKGAGGSAGATTSKSSLGPSALKLLGSAASGK 240

Qy 241 RKESSQSSAQPAKKKSALDEIMELEEEKKRTARTDAWLQPGIVVKIITKKLGEKYHKKK
300 |||||||
Db 241 RKESSQSSAQPAKKKSALDEIMELEEEKKRTARTDAWLQPGIVVKIITKKLGEKYHKKK
300 |||||||
Qy 301 GVVKEVIDRYTAVVKMTDGDRLKLDQTHLETVIPAPGKRVVLVNGGYRGNEGTLESINE
360 |||||||
Db 301 GVVKEVIDRYTAVVKMTDGDRLKLDQTHLETVIPAPGKRVVLVNGGYRGNEGTLESINE
360 |||||||
Qy 361 KAFSATIVIETGPLKGRRVEGIQYEDISKLA 391
Db 361 KAFSATIVIETGPLKGRRVEGIQYEDISKLA 391